preferably predicted and screened, based on primer design software corresponding to the partial sequence designing processors 403-415 in Fig. 4. The partial sequence designing conditions were as follows.

(1)   base length: 20 to 28 bps;

(2)   GC content: 50 to 60%:

(3)   Tm: 50 to 80°C; |TM| : below 20°C; and

(4)   located as close as possible to the 5' end or 3' end.

Pattern II

For pattern II, exons were screened, and primers were then designed. For pattern II, exons were screened based on selected conditions from previously prepared exon database 307, then the template DNA sequence A1 (i.e., a screened exon) was transferred through the input 4-1 to the partial sequence designing processors 403-415 in Fig. 4 suvh that the process for designing partial sequences was run based on primer design software. The exon screening conditions are given below. The partial sequence designing conditions were the same as for pattern I.

(1)   exon length: 300 bps or less

(2)   exons predicted by an exon predicting program

(3)   found in EST database, and expression confirmed

(4)   unknown function (not found in protein database)

(5)   SNP potential (variation in EST database)

Pattern III

After the exon prediction, exons were screened, and primers were then designed. For pattern III, exons were predicted using software corresponding to the exon predicting program

2

304 from genomic DNA sequences 303, the output exon sequences 305 were compiled into a database 307 through a sequence input interface 306, exons were screened in the exon database 307 on the basis of the set conditions, then the template DNA sequence A1 (i.e., a predicted then screened exon) was transferred through the input 401 to the partial sequence designing processors 403-415 in Fig. 4 such that the process for designing partial sequences was run by primer design software. The exon screening conditions were the same as for pattern II. The partial sequence extraction conditions were the same as for pattern I.

Table 1 shows the results of calculations for the time needed to run patterns I through III one thousand times, respectively. In Table 1, "T1" represents that time (minutes) needed for exon prediction, "T2" represents the time (minutes) needed for exon screening, and "T3" represents the time (minutes) needed for primer design.

Table 1

	I	II	III
T1 (min)	0	0	1244.8
T2 (min)	0	598.2	598.2
T3 (min)	49.8	49.8	49.8
Calculated time (min) needed to design 1000 primers	49.8	648 (10.8 H)	1892.8 (31.55 H)
When simultaneously treated by parallel processes (here, 50) by parallel and distributed computers	1.0	13.0	37.9